Alpha Virus nsp4 alignment

CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp4    ------YIFSSDTGSGHLQQKSVRQHNLQCAQLDAVQEEKMYPPKLDTEREKLLLLKMQM 54
RRV_nsp4    ------YIFSSDTGPGHLQQKSVRQHALPCEMLYAHEEERTYPPALDEAREKLLQAKMQM 54
ONV_nsp4    ------YIFSSDTGQGHLQQKSVRQTTLPVNIVEEVHEEKCYPPKLDEIKEQLLLKRLQE 54
SinV_nsp4   LTGVGGYIFSTDTGPGHLQKKSVLQNQLTEPTLERNVLERIHAPVLDTSKEEQLKLRYQM 60
VEEV_nsp4   ------YIFSSDTGQGHLQQKSVRQTVLSEVVLERTELEISYAPRLDQEKEELLRKKLQL 54
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SFV_nsp4    HPSEANKSRYQSRKVENMKATVVDRLTSGARLYTGADVGRIPTYAVRYPRPVYSPTVIER 114
RRV_nsp4    APTEANKSRYQSRKVENMKAVIIDRLKDGARTYLAEQSEKIPTYASKYPRPVYSPSVEDS 114
ONV_nsp4    SASTANRSRYQSRKVENMKATIIHRLKEGCRLYLASETPRVPSYRVTYPAPIYSPSINIK 114
SinV_nsp4   MPTEANKSRYQSRKVENQKAITTERLLSGLRLYNS-ATDQPECYKITYPKPLYSSSVPAN 119
VEEV_nsp4   NPTPANRSRYQSRRVENMKAITARRILQGLGHYLK-AEGKVECYRTLHPVPLYSSSVNRA 113
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SFV_nsp4    FSSPDVAIAACNEYLSRNYPTVASYQITDEYDAYLDMVDGSDSCLDRATFCPAKLRCYPK 174
RRV_nsp4    LQSPEVAVAACNAFLEANYPTVASYQITDEYDAYLDMVDGSESCLDRATFCPAKLRCYPK 174
ONV_nsp4    LTNPETAVAVCNEFLARNYPTVASYQVTDEYDAYLDMVDGSESCLDRATFNPSKLRSYPK 174
SinV_nsp4   YSDPQFAVAVCNNYLHENYPTVASYQITDEYDAYLDMVDGTVACLDTATFCPAKLRSYPK 179
VEEV_nsp4   FSSPKVAVEACNAMLKENFPTVASYCIIPEYDAYLDMVDGASCCLDTASFCPAKLRSFPK 173
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SFV_nsp4    HHAYHQPTVRSAVPSPFQNTLQNVLAAATKRNCNVTQMRELPTMDSAVFNVECFKRYACS 234
RRV_nsp4    HHAYHQPQVRSAVPSPFQNTLQNVLAAATKRNCNVTQMRELPTLDSAVFNVECFKKFACN 234
ONV_nsp4    QHSYHAPTIRSAVPSPFQNTLQNVLAAATKRNCNVTQMRELPTMDSAVFNVECFKKYACN 234
SinV_nsp4   KHEYRAPNIRSAVPSAMQNTLQNVLIAATKRNCNVTQMRELPTLDSATFNVECFRKYACN 239
VEEV_nsp4   KHSYLEPTIRSAVPSAIQNTLQNVLAAATKRNCNVTQMRELPVLDSAAFNVECFKKYACN 233
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SFV_nsp4    GEYWEEYAKQPIRITTENITTYVTKLKGPKAAALFAKTHNLVPLQEVPMDRFTVDMKRDV 294
RRV_nsp4    GEYWQEFKDDPIRITTENITTYVTRLKGPKAAALFAKTHNLVPLQEVPMDRFVVDMKRDV 294
ONV_nsp4    QEYWREFASSPIRVTTENLTMYVTKLKGPKAAALFAKTHNLLPLQEVPMDRFTMDMKRDV 294
SinV_nsp4   DEYWEFARKPIRITTEFVTAYVARLKGPKAAALFAKTYNLVPLQEVPMDRFVMDMKRDV 299
VEEV_nsp4   NEYWETFKENPIRLTEENVVNYITKLKGPKAAALFAKTHNLNMLQDIPMDRFVMDLKRDV 293
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SFV_nsp4    KVTPGTKHTEERPKVQVIQAAEPLATAYLCGIHRELVRRLNAVLRPNVHTLFDMSAEDFD 354
RRV_nsp4    KVTPGTKHTEERPKVQVIQAAEPLATAYLCGIHRELVRRLKAVLAPNIHTLFDMSAEDFD 354
ONV_nsp4    KVTPGTKHTEERPKVQVIQAAEPLATAYLCGIHRELVRRLNAVLLPNVHTLFDMSAEDFD 354
SinV_nsp4   KVTPGTKHTEERPKVQVIQAAEPLATAYLCGIHRELVRRLTAVLLPNIHTLFDMSAEDFD 359
VEEV_nsp4   KVTPGTKHTEERPKVQVIQAADPLATADLCGIHRELVRRLNAVLLPNIHTLFDMSAEDFD 353
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SFV_nsp4    AIIASHFHPGDPVLETDIASFDKSQDDSLALTGLMILEDLGVDQYLLDLIEAAFGEISSC 414
RRV_nsp4    AIIAAHFQPGDAVLETDIASFDKSQDDSLALTALMLLEDLGVDQELLDLIEEAFGEITSV 414
ONV_nsp4    AIIATHFKPGDAVLETDIASFDKSQDDSLASTAMMLLEDLGVDQPILDLIEAAFGEISSC 414
SinV_nsp4   AIIAEHFKQGDPVLETDIASFDKSQDDAMALTGLMILEDLGVDQPLLDLIECAFGEISST 419
VEEV_nsp4   AIIAEHFQPGDCVLETDIASFDKSEDDAMALTALMILEDLGVDAELLTLIEAAFGEISSI 413
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SFV_nsp4    HLPTGTRFKFGAMMKSGMFLTLFINTVLNITIASRVLEQRLTDSACAAFIGDDNIVHGVI 474
RRV_nsp4    HLPTGTRFKFGAMMKSGMFLTLFINTLLNIVIACRVLREKLTNSICAAFIGDDNIVHGVR 474
ONV_nsp4    HLPTGTRFKFGAMMKSGMFLTLFVNTLLNITIASRVLEERLTTSACAAFIGDDNIIHGVV 474
SinV_nsp4   HLPTGTRFKFGAMMKSGMFLTLFVNTVLNVVIASRVLEERLKTSRCAAFIGDDNIIHGVV 479
VEEV_nsp4   HLPTKTKFKFGAMMKSGMFLTLFVNTVINIVIASRVLRERLTGSPCAAFIGDDNIVKGVK 473
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SFV_nsp4    SDKLMAERCASWVNMEVKIIDAVMGEKPPYFCGGFIVFDSVTQTACRVSDPLKRLFKLGK 534
RRV_nsp4    SDPLMAERCASWVNMEVKIIDATMCEKPPYFCGGFILYDNVTGSACRVADPLKRLFKLGK 534
ONV_nsp4    SDALMAARCATWMNMEVKIIDAVVSEKAPYFCGGFILHDTVTGTSCRVADPLKRLFKLGK 534
SinV_nsp4   SDKEMAERCATWLNMEVKIIDAVIGERPPYFCGGFILQDSVTSTACRVADPLKRLFKLGK 539
VEEV_nsp4   SDKLMADRCATWLNMEVKIIDAVVGEKAPYFCGGFILCDSVTGTACRVADPLKRLFKLGK 533
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SFV_nsp4     PLTAEDKQDEDRRRALSDEVSKWFRTGLGAELEVALTSRYEVEGCKSILIAMTTLARDIK  594
RRV_nsp4     PLPAGDTQDEDRRRALKDETDRWARVGLKSELEIALSSRYEVNGTGNIVRAMATLAKSLK  594
ONV_nsp4     PLAAGDEQDEDRRRALADEVTRWQRTGLVTELEKAVYSRYEVQGITAVITSMATFANSKE  594
SinV_nsp4    PLPADDEQDEDRRRALLDETKAWFRVGITGTLAVAVTTRYEVDNITPVLLALRTFAQSKR  599
VEEV_nsp4    PLAVDDEHDDDRRRALHEESTRWNRVGILPELCKAVESRYETVGTSIIVMAMTTLASSVK  593
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SFV_nsp4     AFKKLRGPVIHLYGGPRLVR  614
RRV_nsp4     NFKKLRGPIVHLYGGPK---  611
ONV_nsp4     NFKKLRGPVVTLYGGPK---  611
SinV_nsp4    AFQAIRGEIKHLYGGPK---  616
VEEV_nsp4    SFSYLRGAPITLY------  606
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